

REMARKS

Claims 1, 2, 4, 10 – 12, 14 – 16, 19, 20, 67, 70 – 73, and 75 – 78 were pending in the application. The Examiner has withdrawn claims 71, 73, and 77 from consideration and has deemed claims 60, 70, and 72 allowed. By way of this amendment, claim 1 is amended.

Claim 1 has been amended for clarity and to correct a typographical error noted by Applicants.

The amendments to the claims are made solely to obtain expeditious allowance of the instant application and not for reasons related to patentability. Amendment of the claims is made without prejudice, without intent to abandon any originally claimed subject matter, and without intent to acquiesce in any rejection of record. Applicants expressly reserve the right to file one or more continuing applications hereof containing the canceled or unamended claims. Support for the amendments to the claims can be found throughout the specification and in the originally filed claims, for example in paragraph 55 of the published application. No new matter has been added by these amendments and the Examiner is respectfully requested to enter them. Upon entry of this amendment, claims 1, 2, 4, 10 – 12, 14 – 16, 19, 20, 67, 70 – 73, and 75 – 78 will be pending.

RESPONSE TO THE REJECTIONS**Rejections under 35 U.S.C. §112, second paragraph**

A. Claims 1, 2, 4, 10 – 12, 14 – 16, 19, 20, 75, 76 and 78 were rejected under 35 U.S.C. §112, second paragraph as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The Examiner alleges that claims 1, 2, 4, 10 – 12, 14 – 16, 19, 20, 75, 76 and 78 are unclear as to whether the at least one artificially mutated nucleotide is relative to a fragment of or the full-length SEQ ID NO:1. Claim 1 has been amended to recite “relative to SEQ ID NO:1”, thus clarifying that the isolated or recombinant nucleic acid comprises at least one artificially mutated nucleotide relative to the full-length sequence of SEQ ID NO:1.

In view of the presently amended Claim 1, it is believed that this rejection is now moot and Applicants respectfully request that the rejection of claims 2, 4, 10 – 12, 14 – 16, 19, 20, 75, 76 and 78 under 35 U.S.C. 112, 2nd paragraph be withdrawn.

B. Claims 14 and 15 were rejected under 35 U.S.C. §112, second paragraph as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Briefly, the Examiner alleges that claims 14 and 15 are unclear because a sequence lacking the entire reading frame encoded by either SEQ ID NO:10 or SEQ ID NO:12 is not likely to be greater than 97.8% identical to SEQ ID NO:1.

Applicants respectfully disagree.

Applicants respectfully assert that, contrary to the Examiner’s interpretation, the deletion of either SEQ ID NO:10, SEQ ID NO:12 or the amino acid residues 164 – 197 of SEQ ID NO:12 results in a claim that is clearly defined. Newly amended Claim 1 recites in part:

An isolated or recombinant nucleic acid comprising at least one artificially mutated nucleotide relative to SEQ ID NO: 1 ..., wherein the mutated nucleotide comprises one or more of: a deleted nucleotide, an inserted nucleotide, or a substituted nucleotide, and wherein the nucleic acid comprises:

(a) a polynucleotide sequence that is greater than 97.8% identical to SEQ ID NO: 1 ... **or**

(b) a polynucleotide sequence encoding an amino acid sequence or unique subsequence selected from the group consisting of....

Thus, Claim 1 does not require that the sequence be greater than 97.8% identical to SEQ ID NO:1, the sequence could also satisfy one of the Markush grouping of amino acid sequences set out in part b).

Deletion of the open reading frame encoding SEQ ID NO:10 (the M2-2 protein which is 93 amino acids in length; encoded by 279 nucleotides) would remove 1.83% of the nucleotides of SEQ ID NO:1 (15,225 nucleotides in length), resulting in an isolated or recombinant nucleic acid comprising at least one artificially mutated nucleotide relative to SEQ ID NO:1 or its complement, wherein the nucleic acid comprises a polynucleotide sequence that is 98.17% identical to SEQ ID NO:1. While deletion of the open reading frame encoding SEQ ID NO:12 (the G protein which is 292 amino acids in length; encoded by 876 nucleotides) would remove 5.75% of the nucleotides of SEQ ID NO:1, it would still result in an isolated or recombinant nucleic acid comprising at least one artificially mutated nucleotide relative to SEQ ID NO:1 or its complement. While deletion of the entire open reading frame encoding SEQ ID NO:12 from SEQ ID NO:1 would result in a nucleic acid having only 94.25% identity to SEQ ID NO:1, Applicants submit that deletion of the entire open reading frame encoding SEQ ID NO:12 would still render Claim 14 definite when read in the context of the comprising language of claim 1 under part (b). Applicants further submit that claim 14 is definite and distinctly points out the subject matter Applicants regard as their invention in that deletion of either the open reading frame of SEQ ID NO:10 or the open reading frame of SEQ ID NO:12 clearly defines the artificially mutated nucleotide limitation for the nucleic acid sequence of claim 1.

Claim 15 recites that the at least one artificially mutated nucleotide is a deletion, and further that it is the nucleotides encoding amino acid residues 164 – 197 of SEQ ID NO:12 that are deleted. Deletion of the nucleotides encoding amino acid residues 164 – 197 of SEQ ID NO:12 would remove 102 nucleotides (encoding 34 amino acid residues) from the nucleic acid of claim 1. With respect to SEQ ID NO:1, this would be a reduction of 0.67% of the nucleotides, resulting in an isolated or recombinant nucleic acid comprising at least one artificially mutated nucleotide relative to SEQ ID NO:1 or its complement, wherein the nucleic acid comprises a polynucleotide sequence that is 99.33% identical to SEQ ID NO:1. Therefore, claim 15 is

definite and distinctly points out the subject matter Applicants regard as their invention in that deletion of the nucleotides encoding amino acid residues 164 – 197 of SEQ ID NO:12 clearly defines the artificially mutated nucleotide limitations for the nucleic acid sequence of claims 12 and 1.

In view of the above remarks, Applicants respectfully request that the rejection under of Claims 14 and 15 35 U.S.C. §112, second paragraph be withdrawn.

Conclusion

In view of the foregoing amendments and remarks, Applicants submit that the claims currently under consideration by the Examiner (1, 2, 4, 10 – 12, 14 – 16, 19, 20, 67, 70, 72, 75, 76, and 78) are in condition for allowance. A notice of allowance is earnestly solicited. The Examiner may call the undersigned at 302-885-9129, if a telephonic interview would be helpful.

Respectfully submitted,

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/Robin S. QUARTIN, Reg. No. 45,028/
Robin S. Quartin, Ph.D.
Attorney for Applicant
Registration No. 45,028
(302) 885-9129